



SEQUENCE LISTING

<110> Chan, Doug W
Chen, Ping-Chi B
Chen, David J

<120> DNA Dependent Protein Kinase Catalytic Subunit Phosphorylation Sites
and Antibodies Thereto

<130> IB-1807 PCT

<140> US 10/511,561

<141> 2004-10-15

<150> US 60/375,094

<151> 2002-04-22

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<170> PatentIn version 3.1

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<223> HUMAN GENETIC ORIGIN

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<213> Homo sapiens

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Gln Leu Ile Arg Gly Leu Gly Gln Glu Cys Val Leu Ser Ser Ser Pro
35 40 45

Ala Val Leu Ala Leu Gln Thr Ser Leu Val Phe Ser Arg Asp Phe Gly
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Leu Leu Val Phe Val Arg Lys Ser Leu Asn Ser Ile Glu Phe Arg Glu
65 70 75 80

Cys Arg Glu Glu Ile Leu Lys Phe Leu Cys Ile Phe Leu Glu Lys Met
85 90 95

Gly Gln Lys Ile Ala Pro Tyr Ser Val Glu Ile Lys Asn Thr Cys Thr
100 105 110

Ser Val Tyr Thr Lys Asp Arg Ala Ala Lys Cys Lys Ile Pro Ala Leu
115 120 125

Asp Leu Leu Ile Lys Leu Leu Gln Thr Phe Arg Ser Ser Arg Leu Met
130 135 140

Asp Glu Phe Lys Ile Gly Glu Leu Phe Ser Lys Phe Tyr Gly Glu Leu
145 150 155 160

Ala Leu Lys Lys Lys Ile Pro Asp Thr Val Leu Glu Lys Val Tyr Glu
165 170 175

Leu Leu Gly Leu Leu Gly Glu Val His Pro Ser Glu Met Ile Asn Asn
180 185 190

Ala Glu Asn Leu Phe Arg Ala Phe Leu Gly Glu Leu Lys Thr Gln Met
195 200 205

Thr Ser Ala Val Arg Glu Pro Lys Leu Pro Val Leu Ala Gly Cys Leu
210 215 220

Lys Gly Leu Ser Ser Leu Leu Cys Asn Phe Thr Lys Ser Met Glu Glu
225 230 235 240

Asp Pro Gln Thr Ser Arg Glu Ile Phe Asn Phe Val Leu Lys Ala Ile
245 250 255

Arg Pro Gln Ile Asp Leu Lys Arg Tyr Ala Val Pro Ser Ala Gly Leu
260 265 270

Arg Leu Phe Ala Leu His Ala Ser Gln Phe Ser Thr Cys Leu Leu Asp
275 280 285

Asn Tyr Val Ser Leu Phe Glu Val Leu Leu Lys Trp Cys Ala His Thr
290 295 300

Asn Val Glu Leu Lys Lys Ala Ala Leu Ser Ala Leu Glu Ser Phe Leu
305 310 315 320

Lys Gln Val Ser Asn Met Val Ala Lys Asn Ala Glu Met His Lys Asn
325 330 335

Lys Leu Gln Tyr Phe Met Glu Gln Phe Tyr Gly Ile Ile Arg Asn Val
340 345 350

Asp Ser Asn Asn Lys Glu Leu Ser Ile Ala Ile Arg Gly Tyr Gly Leu
355 360 365

Phe Ala Gly Pro Cys Lys Val Ile Asn Ala Lys Asp Val Asp Phe Met
370 375 380

Tyr Val Glu Leu Ile Gln Arg Cys Lys Gln Met Phe Leu Thr Gln Thr
385 390 395 400

Asp Thr Gly Asp Tyr Arg Val Tyr Gln Met Pro Ser Phe Leu Gln Ser
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Val Ala Ser Val Leu Leu Tyr Leu Asp Thr Val Pro Glu Val Tyr Thr
420 425 430

Pro Val Leu Glu His Leu Val Val Met Gln Ile Asp Ser Phe Pro Gln
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Tyr Ser Pro Lys Met Gln Leu Val Cys Cys Arg Ala Ile Val Lys Val
450 455 460

Phe Leu Ala Leu Ala Ala Lys Gly Pro Val Leu Arg Asn Cys Ile Ser
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Thr Val Val His Gln Gly Leu Ile Arg Ile Cys Ser Lys Pro Val Val
485 490 495

Leu Pro Lys Gly Pro Glu Ser Glu Ser Glu Asp His Arg Ala Ser Gly
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Glu Val Arg Thr Gly Lys Trp Lys Val Pro Thr Tyr Lys Asp Tyr Val
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Asp Leu Phe Arg His Leu Leu Ser Ser Asp Gln Met Met Asp Ser Ile
530 535 540

Leu Ala Asp Glu Ala Phe Phe Ser Val Asn Ser Ser Ser Glu Ser Leu
545 550 555 560

Asn His Leu Leu Tyr Asp Glu Phe Val Lys Ser Val Leu Lys Ile Val
565 570 575

Glu Lys Leu Asp Leu Thr Leu Glu Ile Gln Thr Val Gly Glu Gln Glu
580 585 590

Asn Gly Asp Glu Ala Pro Gly Val Trp Met Ile Pro Thr Ser Asp Pro
595 600 605

Ala Ala Asn Leu His Pro Ala Lys Pro Lys Asp Phe Ser Ala Phe Ile
610 615 620

Asn Leu Val Glu Phe Cys Arg Glu Ile Leu Pro Glu Lys Gln Ala Glu
625 630 635 640

Phe Phe Glu Pro Trp Val Tyr Ser Phe Ser Tyr Glu Leu Ile Leu Gln
645 650 655

Ser Thr Arg Leu Pro Leu Ile Ser Gly Phe Tyr Lys Leu Leu Ser Ile
660 665 670

Thr Val Arg Asn Ala Lys Lys Ile Lys Tyr Phe Glu Gly Val Ser Pro
675 680 685

Lys Ser Leu Lys His Ser Pro Glu Asp Pro Glu Lys Tyr Ser Cys Phe
690 695 700

Ala Leu Phe Val Lys Phe Gly Lys Glu Val Ala Val Lys Met Lys Gln
705 710 715 720

Tyr Lys Asp Glu Leu Leu Ala Ser Cys Leu Thr Phe Leu Leu Ser Leu
725 730 735

Pro His Asn Ile Ile Glu Leu Asp Val Arg Ala Tyr Val Pro Ala Leu
740 745 750

Gln Met Ala Phe Lys Leu Gly Leu Ser Tyr Thr Pro Leu Ala Glu Val
755 760 765

Gly Leu Asn Ala Leu Glu Glu Trp Ser Ile Tyr Ile Asp Arg His Val
770 775 780

Met Gln Pro Tyr Tyr Lys Asp Ile Leu Pro Cys Leu Asp Gly Tyr Leu
785 790 795 800

Lys Thr Ser Ala Leu Ser Asp Glu Thr Lys Asn Asn Trp Glu Val Ser
805 810 815

Ala Leu Ser Arg Ala Ala Gln Lys Gly Phe Asn Lys Val Val Leu Lys
820 825 830

His Leu Lys Lys Thr Lys Asn Leu Ser Ser Asn Glu Ala Ile Ser Leu
835 840 845

Glu Glu Ile Arg Ile Arg Val Val Gln Met Leu Gly Ser Leu Gly Gly
850 855 860

Gln Ile Asn Lys Asn Leu Leu Thr Val Thr Ser Ser Asp Glu Met Met
865 870 875 880

Lys Ser Tyr Val Ala Trp Asp Arg Glu Lys Arg Leu Ser Phe Ala Val
885 890 895

Pro Phe Arg Glu Met Lys Pro Val Ile Phe Leu Asp Val Phe Leu Pro
900 905 910

Arg Val Thr Glu Leu Ala Leu Thr Ala Ser Asp Arg Gln Thr Lys Val

915

920

925

Ala Ala Cys Glu Leu Leu His Ser Met Val Met Phe Met Leu Gly Lys
 930 935 940

Ala Thr Gln Met Pro Glu Gly Gly Gln Gly Ala Pro Pro Met Tyr Gln
 945 950 955 960

Leu Tyr Lys Arg Thr Phe Pro Val Leu Leu Arg Leu Ala Cys Asp Val
 965 970 975

Asp Gln Val Thr Arg Gln Leu Tyr Glu Pro Leu Val Met Gln Leu Ile
 980 985 990

His Trp Phe Thr Asn Asn Lys Lys Phe Glu Ser Gln Asp Thr Val Ser
 995 1000 1005

Leu Leu Glu Ala Ile Leu Asp Gly Ile Val Asp Pro Val Asp Ser
 1010 1015 1020

Thr Leu Arg Asp Phe Cys Gly Arg Cys Ile Arg Glu Phe Leu Lys
 1025 1030 1035

Trp Ser Ile Lys Gln Ile Thr Pro Gln Gln Gln Glu Lys Ser Pro
 1040 1045 1050

Val Asn Thr Lys Ser Leu Phe Lys Arg Leu Tyr Ser Leu Ala Leu
 1055 1060 1065

His Pro Asn Ala Phe Lys Arg Leu Gly Ala Ser Leu Ala Phe Asn
 1070 1075 1080

Asn Ile Tyr Arg Glu Phe Arg Glu Glu Glu Ser Leu Val Glu Gln
 1085 1090 1095

Phe Val Phe Glu Ala Leu Val Ile Tyr Met Glu Ser Leu Ala Leu
 1100 1105 1110

Ala His Ala Asp Glu Lys Ser Leu Gly Thr Ile Gln Gln Cys Cys
 1115 1120 1125

Asp Ala Ile Asp His Leu Cys Arg Ile Ile Glu Lys Lys His Val
 1130 1135 1140

Ser Leu Asn Lys Ala Lys Lys Arg Arg Leu Pro Arg Gly Phe Pro
 1145 1150 1155

Pro Ser Ala Ser Leu Cys Leu Leu Asp Leu Val Lys Trp Leu Leu
1160 1165 1170

Ala His Cys Gly Arg Pro Gln Thr Glu Cys Arg His Lys Ser Ile
1175 1180 1185

Glu Leu Phe Tyr Lys Phe Val Pro Leu Leu Pro Gly Asn Arg Ser
1190 1195 1200

Pro Asn Leu Trp Leu Lys Asp Val Leu Lys Glu Glu Gly Val Ser
1205 1210 1215

Phe Leu Ile Asn Thr Phe Glu Gly Gly Gly Cys Gly Gln Pro Ser
1220 1225 1230

Gly Ile Leu Ala Gln Pro Thr Leu Leu Tyr Leu Arg Gly Pro Phe
1235 1240 1245

Ser Leu Gln Ala Thr Leu Cys Trp Leu Asp Leu Leu Leu Ala Ala
1250 1255 1260

Leu Glu Cys Tyr Asn Thr Phe Ile Gly Glu Arg Thr Val Gly Ala
1265 1270 1275

Leu Gln Val Leu Gly Thr Glu Ala Gln Ser Ser Leu Leu Lys Ala
1280 1285 1290

Val Ala Phe Phe Leu Glu Ser Ile Ala Met His Asp Ile Ile Ala
1295 1300 1305

Ala Glu Lys Cys Phe Gly Thr Gly Ala Ala Gly Asn Arg Thr Ser
1310 1315 1320

Pro Gln Glu Gly Glu Arg Tyr Asn Tyr Ser Lys Cys Thr Val Val
1325 1330 1335

Val Arg Ile Met Glu Phe Thr Thr Thr Leu Leu Asn Thr Ser Pro
1340 1345 1350

Glu Gly Trp Lys Leu Leu Lys Lys Asp Leu Cys Asn Thr His Leu
1355 1360 1365

Met Arg Val Leu Val Gln Thr Leu Cys Glu Pro Ala Ser Ile Gly
1370 1375 1380

Phe Asn Ile Gly Asp Val Gln Val Met Ala His Leu Pro Asp Val
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Cys Val Asn Leu Met Lys Ala Leu Lys Met Ser Pro Tyr Lys Asp
1400 1405 1410

Ile Leu Glu Thr His Leu Arg Glu Lys Ile Thr Ala Gln Ser Ile
1415 1420 1425

Glu Glu Leu Cys Ala Val Asn Leu Tyr Gly Pro Asp Ala Gln Val
1430 1435 1440

Asp Arg Ser Arg Leu Ala Ala Val Val Ser Ala Cys Lys Gln Leu
1445 1450 1455

His Arg Ala Gly Leu Leu His Asn Ile Leu Pro Ser Gln Ser Thr
1460 1465 1470

Asp Leu His His Ser Val Gly Thr Glu Leu Leu Ser Leu Val Tyr
1475 1480 1485

Lys Gly Ile Ala Pro Gly Asp Glu Arg Gln Cys Leu Pro Ser Leu
1490 1495 1500

Asp Leu Ser Cys Lys Gln Leu Ala Ser Gly Leu Leu Glu Leu Ala
1505 1510 1515

Phe Ala Phe Gly Gly Leu Cys Glu Arg Leu Val Ser Leu Leu Leu
1520 1525 1530

Asn Pro Ala Val Leu Ser Thr Ala Ser Leu Gly Ser Ser Gln Gly
1535 1540 1545

Ser Val Ile His Phe Ser His Gly Glu Tyr Phe Tyr Ser Leu Phe
1550 1555 1560

Ser Glu Thr Ile Asn Thr Glu Leu Leu Lys Asn Leu Asp Leu Ala
1565 1570 1575

Val Leu Glu Leu Met Gln Ser Ser Val Asp Asn Thr Lys Met Val
1580 1585 1590

Ser Ala Val Leu Asn Gly Met Leu Asp Gln Ser Phe Arg Glu Arg
1595 1600 1605

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Gln	His	Trp	Lys	Lys	Cys	Asp	Ser	Trp	Trp	Ala	Lys	Asp	Ser	Pro
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Leu	Glu	Thr	Lys	Met	Ala	Val	Leu	Ala	Leu	Leu	Ala	Lys	Ile	Leu
1640						1645					1650			
Gln	Ile	Asp	Ser	Ser	Val	Ser	Phe	Asn	Thr	Ser	His	Gly	Ser	Phe
1655						1660					1665			
Pro	Glu	Val	Phe	Thr	Thr	Tyr	Ile	Ser	Leu	Leu	Ala	Asp	Thr	Lys
1670						1675					1680			
Leu	Asp	Leu	His	Leu	Lys	Gly	Gln	Ala	Val	Thr	Leu	Leu	Pro	Phe
1685						1690					1695			
Phe	Thr	Ser	Leu	Thr	Gly	Gly	Ser	Leu	Glu	Glu	Leu	Arg	Arg	Val
1700						1705					1710			
Leu	Glu	Gln	Leu	Ile	Val	Ala	His	Phe	Pro	Met	Gln	Ser	Arg	Glu
1715						1720					1725			
Phe	Pro	Pro	Gly	Thr	Pro	Arg	Phe	Asn	Asn	Tyr	Val	Asp	Cys	Met
1730						1735					1740			
Lys	Lys	Phe	Leu	Asp	Ala	Leu	Glu	Leu	Ser	Gln	Ser	Pro	Met	Leu
1745						1750					1755			
Leu	Glu	Leu	Met	Thr	Glu	Val	Leu	Cys	Arg	Glu	Gln	Gln	His	Val
1760						1765					1770			
Met	Glu	Glu	Leu	Phe	Gln	Ser	Ser	Phe	Arg	Arg	Ile	Ala	Arg	Arg
1775						1780					1785			
Gly	Ser	Cys	Val	Thr	Gln	Val	Gly	Leu	Leu	Glu	Ser	Val	Tyr	Glu
1790						1795					1800			
Met	Phe	Arg	Lys	Asp	Asp	Pro	Arg	Leu	Ser	Phe	Thr	Arg	Gln	Ser
1805						1810					1815			
Phe	Val	Asp	Arg	Ser	Leu	Leu	Thr	Leu	Leu	Trp	His	Cys	Ser	Leu
1820						1825					1830			
Asp	Ala	Leu	Arg	Glu	Phe	Phe	Ser	Thr	Ile	Val	Val	Asp	Ala	Ile

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Asp	Thr	Gln	Ile	Thr	Lys	Lys	Met	Gly	Tyr	Tyr	Lys	Ile	Leu	Asp
1865						1870					1875			
Val	Met	Tyr	Ser	Arg	Leu	Pro	Lys	Asp	Asp	Val	His	Ala	Lys	Glu
1880						1885					1890			
Ser	Lys	Ile	Asn	Gln	Val	Phe	His	Gly	Ser	Cys	Ile	Thr	Glu	Gly
1895						1900					1905			
Asn	Glu	Leu	Thr	Lys	Thr	Leu	Ile	Lys	Leu	Cys	Tyr	Asp	Ala	Phe
1910						1915					1920			
Thr	Glu	Asn	Met	Ala	Gly	Glu	Asn	Gln	Leu	Leu	Glu	Arg	Arg	Arg
1925						1930					1935			
Leu	Tyr	His	Cys	Ala	Ala	Tyr	Asn	Cys	Ala	Ile	Ser	Val	Ile	Cys
1940						1945					1950			
Cys	Val	Phe	Asn	Glu	Leu	Lys	Phe	Tyr	Gln	Gly	Phe	Leu	Phe	Ser
1955						1960					1965			
Glu	Lys	Pro	Glu	Lys	Asn	Leu	Leu	Ile	Phe	Glu	Asn	Leu	Ile	Asp
1970						1975					1980			
Leu	Lys	Arg	Arg	Tyr	Asn	Phe	Pro	Val	Glu	Val	Glu	Val	Pro	Met
1985						1990					1995			
Glu	Arg	Lys	Lys	Lys	Tyr	Ile	Glu	Ile	Arg	Lys	Glu	Ala	Arg	Glu
2000						2005					2010			
Ala	Ala	Asn	Gly	Asp	Ser	Asp	Gly	Pro	Ser	Tyr	Met	Ser	Ser	Leu
2015						2020					2025			
Ser	Tyr	Leu	Ala	Asp	Ser	Thr	Leu	Ser	Glu	Glu	Met	Ser	Gln	Phe
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Asp	Phe	Ser	Thr	Gly	Val	Gln	Ser	Tyr	Ser	Tyr	Ser	Ser	Gln	Asp
2045						2050					2055			
Pro	Arg	Pro	Ala	Thr	Gly	Arg	Phe	Arg	Arg	Arg	Glu	Gln	Arg	Asp
2060						2065					2070			

Pro Thr Val His Asp Asp Val Leu Glu Leu Glu Met Asp Glu Leu
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Asn Arg His Glu Cys Met Ala Pro Leu Thr Ala Leu Val Lys His
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Met His Arg Ser Leu Gly Pro Pro Gln Gly Glu Glu Asp Ser Val
2105 2110 2115

Pro Arg Asp Leu Pro Ser Trp Met Lys Phe Leu His Gly Lys Leu
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Gly Asn Pro Ile Val Pro Leu Asn Ile Arg Leu Phe Leu Ala Lys
2135 2140 2145

Leu Val Ile Asn Thr Glu Glu Val Phe Arg Pro Tyr Ala Lys His
2150 2155 2160

Trp Leu Ser Pro Leu Leu Gln Leu Ala Ala Ser Glu Asn Asn Gly
2165 2170 2175

Gly Glu Gly Ile His Tyr Met Val Val Glu Ile Val Ala Thr Ile
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Leu Ser Trp Thr Gly Leu Ala Thr Pro Thr Gly Val Pro Lys Asp
2195 2200 2205

Glu Val Leu Ala Asn Arg Leu Leu Asn Phe Leu Met Lys His Val
2210 2215 2220

Phe His Pro Lys Arg Ala Val Phe Arg His Asn Leu Glu Ile Ile
2225 2230 2235

Lys Thr Leu Val Glu Cys Trp Lys Asp Cys Leu Ser Ile Pro Tyr
2240 2245 2250

Arg Leu Ile Phe Glu Lys Phe Ser Gly Lys Asp Pro Asn Ser Lys
2255 2260 2265

Asp Asn Ser Val Gly Ile Gln Leu Leu Gly Ile Val Met Ala Asn
2270 2275 2280

Asp Leu Pro Pro Tyr Asp Pro Gln Cys Gly Ile Gln Ser Ser Glu
2285 2290 2295

Tyr Phe Gln Ala Leu Val Asn Asn Met Ser Phe Val Arg Tyr Lys
2300 2305 2310

Glu Val Tyr Ala Ala Ala Ala Glu Val Leu Gly Leu Ile Leu Arg
2315 2320 2325

Tyr Val Met Glu Arg Lys Asn Ile Leu Glu Glu Ser Leu Cys Glu
2330 2335 2340

Leu Val Ala Lys Gln Leu Lys Gln His Gln Asn Thr Met Glu Asp
2345 2350 2355

Lys Phe Ile Val Cys Leu Asn Lys Val Thr Lys Ser Phe Pro Pro
2360 2365 2370

Leu Ala Asp Arg Phe Met Asn Ala Val Phe Phe Leu Leu Pro Lys
2375 2380 2385

Phe His Gly Val Leu Lys Thr Leu Cys Leu Glu Val Val Leu Cys
2390 2395 2400

Arg Val Glu Gly Met Thr Glu Leu Tyr Phe Gln Leu Lys Ser Lys
2405 2410 2415

Asp Phe Val Gln Val Met Arg His Arg Asp Asp Glu Arg Gln Lys
2420 2425 2430

Val Cys Leu Asp Ile Ile Tyr Lys Met Met Pro Lys Leu Lys Pro
2435 2440 2445

Val Glu Leu Arg Glu Leu Leu Asn Pro Val Val Glu Phe Val Ser
2450 2455 2460

His Pro Ser Thr Thr Cys Arg Glu Gln Met Tyr Asn Ile Leu Met
2465 2470 2475

Trp Ile His Asp Asn Tyr Arg Asp Pro Glu Ser Glu Thr Asp Asn
2480 2485 2490

Asp Ser Gln Glu Ile Phe Lys Leu Ala Lys Asp Val Leu Ile Gln
2495 2500 2505

Gly Leu Ile Asp Glu Asn Pro Gly Leu Gln Leu Ile Ile Arg Asn
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Phe Trp Ser His Glu Thr Arg Leu Pro Ser Asn Thr Leu Asp Arg
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Leu Leu Ala Leu Asn Ser Leu Tyr Ser Pro Lys Ile Glu Val His
2540 2545 2550

Phe Leu Ser Leu Ala Thr Asn Phe Leu Leu Glu Met Thr Ser Met
2555 2560 2565

Ser Pro Asp Tyr Pro Asn Pro Met Phe Glu His Pro Leu Ser Glu
2570 2575 2580

Cys Glu Phe Gln Glu Tyr Thr Ile Asp Ser Asp Trp Arg Phe Arg
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Ser Thr Val Leu Thr Pro Met Phe Val Glu Thr Gln Ala Ser Gln
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Gly Thr Leu Gln Thr Arg Thr Gln Glu Gly Ser Leu Ser Ala Arg
2615 2620 2625

Trp Pro Val Ala Gly Gln Ile Arg Ala Thr Gln Gln Gln His Asp
2630 2635 2640

Phe Thr Leu Thr Gln Thr Ala Asp Gly Arg Ser Ser Phe Asp Trp
2645 2650 2655

Leu Thr Gly Ser Ser Thr Asp Pro Leu Val Asp His Thr Ser Pro
2660 2665 2670

Ser Ser Asp Ser Leu Leu Phe Ala His Lys Arg Ser Glu Arg Leu
2675 2680 2685

Gln Arg Ala Pro Leu Lys Ser Val Gly Pro Asp Phe Gly Lys Lys
2690 2695 2700

Arg Leu Gly Leu Pro Gly Asp Glu Val Asp Asn Lys Val Lys Gly
2705 2710 2715

Ala Ala Gly Arg Thr Asp Leu Leu Arg Leu Arg Arg Arg Phe Met
2720 2725 2730

Arg Asp Gln Glu Lys Leu Ser Leu Met Tyr Ala Arg Lys Gly Val
2735 2740 2745

Ala Glu Gln Lys Arg Glu Lys Glu Ile Lys Ser Glu Leu Lys Met

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Lys Gln Asp Ala Gln Val Val	Leu Tyr Arg Ser Tyr	Arg His Gly		
2765	2770	2775		
Asp Leu Pro Asp Ile Gln Ile	Lys His Ser Ser Leu	Ile Thr Pro		
2780	2785	2790		
Leu Gln Ala Val Ala Gln Arg	Asp Pro Ile Ile Ala	Lys Gln Leu		
2795	2800	2805		
Phe Ser Ser Leu Phe Ser Gly	Ile Leu Lys Glu Met	Asp Lys Phe		
2810	2815	2820		
Lys Thr Leu Ser Glu Lys Asn	Asn Ile Thr Gln Lys	Leu Leu Gln		
2825	2830	2835		
Asp Phe Asn Arg Phe Leu Asn	Thr Thr Phe Ser Phe	Phe Pro Pro		
2840	2845	2850		
Phe Val Ser Cys Ile Gln Asp	Ile Ser Cys Gln His	Ala Ala Leu		
2855	2860	2865		
Leu Ser Leu Asp Pro Ala Ala	Val Ser Ala Gly Cys	Leu Ala Ser		
2870	2875	2880		
Leu Gln Gln Pro Val Gly Ile	Arg Leu Leu Glu Glu	Ala Leu Leu		
2885	2890	2895		
Arg Leu Leu Pro Ala Glu Leu	Pro Ala Lys Arg Val	Arg Gly Lys		
2900	2905	2910		
Ala Arg Leu Pro Pro Asp Val	Leu Arg Trp Val Glu	Leu Ala Lys		
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Leu Tyr Arg Ser Ile Gly Glu	Tyr Asp Val Leu Arg	Gly Ile Phe		
2930	2935	2940		
Thr Ser Glu Ile Gly Thr Lys	Gln Ile Thr Gln Ser	Ala Leu Leu		
2945	2950	2955		
Ala Glu Ala Arg Ser Asp Tyr	Ser Glu Ala Ala Lys	Gln Tyr Asp		
2960	2965	2970		
Glu Ala Leu Asn Lys Gln Asp	Trp Val Asp Gly Glu	Pro Thr Glu		
2975	2980	2985		

Ala	Glu	Lys	Asp	Phe	Trp	Glu	Leu	Ala	Ser	Leu	Asp	Cys	Tyr	Asn
2990						2995					3000			
His	Leu	Ala	Glu	Trp	Lys	Ser	Leu	Glu	Tyr	Cys	Ser	Thr	Ala	Ser
3005						3010					3015			
Ile	Asp	Ser	Glu	Asn	Pro	Pro	Asp	Leu	Asn	Lys	Ile	Trp	Ser	Glu
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Pro	Phe	Tyr	Gln	Glu	Thr	Tyr	Leu	Pro	Tyr	Met	Ile	Arg	Ser	Lys
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Leu	Lys	Leu	Leu	Leu	Gln	Gly	Glu	Ala	Asp	Gln	Ser	Leu	Leu	Thr
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Phe	Ile	Asp	Lys	Ala	Met	His	Gly	Glu	Leu	Gln	Lys	Ala	Ile	Leu
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Glu	Leu	His	Tyr	Ser	Gln	Glu	Leu	Ser	Leu	Leu	Tyr	Leu	Leu	Gln
3080						3085					3090			
Asp	Asp	Val	Asp	Arg	Ala	Lys	Tyr	Tyr	Ile	Gln	Asn	Gly	Ile	Gln
3095						3100					3105			
Ser	Phe	Met	Gln	Asn	Tyr	Ser	Ser	Ile	Asp	Val	Leu	Leu	His	Gln
3110						3115					3120			
Ser	Arg	Leu	Thr	Lys	Leu	Gln	Ser	Val	Gln	Ala	Leu	Thr	Glu	Ile
3125						3130					3135			
Gln	Glu	Phe	Ile	Ser	Phe	Ile	Ser	Lys	Gln	Gly	Asn	Leu	Ser	Ser
3140						3145					3150			
Gln	Val	Pro	Leu	Lys	Arg	Leu	Leu	Asn	Thr	Trp	Thr	Asn	Arg	Tyr
3155						3160					3165			
Pro	Asp	Ala	Lys	Met	Asp	Pro	Met	Asn	Ile	Trp	Asp	Asp	Ile	Ile
3170						3175					3180			
Thr	Asn	Arg	Cys	Phe	Phe	Leu	Ser	Lys	Ile	Glu	Glu	Lys	Leu	Thr
3185						3190					3195			
Pro	Leu	Pro	Glu	Asp	Asn	Ser	Met	Asn	Val	Asp	Gln	Asp	Gly	Asp
3200						3205					3210			

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Ser Leu Ile Arg Ser Cys Lys Phe Ser Met Lys Met Lys Met Ile
3230 3235 3240

Asp Ser Ala Arg Lys Gln Asn Asn Phe Ser Leu Ala Met Lys Leu
3245 3250 3255

Leu Lys Glu Leu His Lys Glu Ser Lys Thr Arg Asp Asp Trp Leu
3260 3265 3270

Val Ser Trp Val Gln Ser Tyr Cys Arg Leu Ser His Cys Arg Ser
3275 3280 3285

Arg Ser Gln Gly Cys Ser Glu Gln Val Leu Thr Val Leu Lys Thr
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Val Ser Leu Leu Asp Glu Asn Asn Val Ser Ser Tyr Leu Ser Lys
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Asn Ile Leu Ala Phe Arg Asp Gln Asn Ile Leu Leu Gly Thr Thr
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Tyr Arg Ile Ile Ala Asn Ala Leu Ser Ser Glu Pro Ala Cys Leu
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Ala Glu Ile Glu Glu Asp Lys Ala Arg Arg Ile Leu Glu Leu Ser
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Gly Ser Ser Ser Glu Asp Ser Glu Lys Val Ile Ala Gly Leu Tyr
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Gln Arg Ala Phe Gln His Leu Ser Glu Ala Val Gln Ala Ala Glu
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Glu Glu Ala Gln Pro Pro Ser Trp Ser Cys Gly Pro Ala Ala Gly
3395 3400 3405

Val Ile Asp Ala Tyr Met Thr Leu Ala Asp Phe Cys Asp Gln Gln
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Leu Arg Lys Glu Glu Glu Asn Ala Ser Val Thr Asp Ser Ala Glu
3425 3430 3435

Leu Gln Ala Tyr Pro Ala Leu Val Val Glu Lys Met Leu Lys Ala
3440 3445 3450

Leu Lys Leu Asn Ser Asn Glu Ala Arg Leu Lys Phe Pro Arg Leu
3455 3460 3465

Leu Gln Ile Ile Glu Arg Tyr Pro Glu Glu Thr Leu Ser Leu Met
3470 3475 3480

Thr Lys Glu Ile Ser Ser Val Pro Cys Trp Gln Phe Ile Ser Trp
3485 3490 3495

Ile Ser His Met Val Ala Leu Leu Asp Lys Asp Gln Ala Val Ala
3500 3505 3510

Val Gln His Ser Val Glu Glu Ile Thr Asp Asn Tyr Pro Gln Ala
3515 3520 3525

Ile Val Tyr Pro Phe Ile Ile Ser Ser Glu Ser Tyr Ser Phe Lys
3530 3535 3540

Asp Thr Ser Thr Gly His Lys Asn Lys Glu Phe Val Ala Arg Ile
3545 3550 3555

Lys Ser Lys Leu Asp Gln Gly Gly Val Ile Gln Asp Phe Ile Asn
3560 3565 3570

Ala Leu Asp Gln Leu Ser Asn Pro Glu Leu Leu Phe Lys Asp Trp
3575 3580 3585

Ser Asn Asp Val Arg Ala Glu Leu Ala Lys Thr Pro Val Asn Lys
3590 3595 3600

Lys Asn Ile Glu Lys Met Tyr Glu Arg Met Tyr Ala Ala Leu Gly
3605 3610 3615

Asp Pro Lys Ala Pro Gly Leu Gly Ala Phe Arg Arg Lys Phe Ile
3620 3625 3630

Gln Thr Phe Gly Lys Glu Phe Asp Lys His Phe Gly Lys Gly Gly
3635 3640 3645

Ser Lys Leu Leu Arg Met Lys Leu Ser Asp Phe Asn Asp Ile Thr
3650 3655 3660

Asn Met Leu Leu Leu Lys Met Asn Lys Asp Ser Lys Pro Pro Gly

3665							3670									3675
Asn	Leu	Lys	Glu	Cys	Ser	Pro	Trp	Met	Ser	Asp	Phe	Lys	Val	Glu		
3680						3685					3690					
Phe	Leu	Arg	Asn	Glu	Leu	Glu	Ile	Pro	Gly	Gln	Tyr	Asp	Gly	Arg		
3695						3700					3705					
Gly	Lys	Pro	Leu	Pro	Glu	Tyr	His	Val	Arg	Ile	Ala	Gly	Phe	Asp		
3710						3715					3720					
Glu	Arg	Val	Thr	Val	Met	Ala	Ser	Leu	Arg	Arg	Pro	Lys	Arg	Ile		
3725						3730					3735					
Ile	Ile	Arg	Gly	His	Asp	Glu	Arg	Glu	His	Pro	Phe	Leu	Val	Lys		
3740						3745					3750					
Gly	Gly	Glu	Asp	Leu	Arg	Gln	Asp	Gln	Arg	Val	Glu	Gln	Leu	Phe		
3755						3760					3765					
Gln	Val	Met	Asn	Gly	Ile	Leu	Ala	Gln	Asp	Ser	Ala	Cys	Ser	Gln		
3770						3775					3780					
Arg	Ala	Leu	Gln	Leu	Arg	Thr	Tyr	Ser	Val	Val	Pro	Met	Thr	Ser		
3785						3790					3795					
Arg	Leu	Gly	Leu	Ile	Glu	Trp	Leu	Glu	Asn	Thr	Val	Thr	Leu	Lys		
3800						3805					3810					
Asp	Leu	Leu	Leu	Asn	Thr	Met	Ser	Gln	Glu	Glu	Lys	Ala	Ala	Tyr		
3815						3820					3825					
Leu	Ser	Asp	Pro	Arg	Ala	Pro	Pro	Cys	Glu	Tyr	Lys	Asp	Trp	Leu		
3830						3835					3840					
Thr	Lys	Met	Ser	Gly	Lys	His	Asp	Val	Gly	Ala	Tyr	Met	Leu	Met		
3845						3850					3855					
Tyr	Lys	Gly	Ala	Asn	Arg	Thr	Glu	Thr	Val	Thr	Ser	Phe	Arg	Lys		
3860						3865					3870					
Arg	Glu	Ser	Lys	Val	Pro	Ala	Asp	Leu	Leu	Lys	Arg	Ala	Phe	Val		
3875						3880					3885					
Arg	Met	Ser	Thr	Ser	Pro	Glu	Ala	Phe	Leu	Ala	Leu	Arg	Ser	His		
3890						3895					3900					

Phe Ala Ser Ser His Ala Leu Ile Cys Ile Ser His Trp Ile Leu
3905 3910 3915

Gly Ile Gly Asp Arg His Leu Asn Asn Phe Met Val Ala Met Glu
3920 3925 3930

Thr Gly Gly Val Ile Gly Ile Asp Phe Gly His Ala Phe Gly Ser
3935 3940 3945

Ala Thr Gln Phe Leu Pro Val Pro Glu Leu Met Pro Phe Arg Leu
3950 3955 3960

Thr Arg Gln Phe Ile Asn Leu Met Leu Pro Met Lys Glu Thr Gly
3965 3970 3975

Leu Met Tyr Ser Ile Met Val His Ala Leu Arg Ala Phe Arg Ser
3980 3985 3990

Asp Pro Gly Leu Leu Thr Asn Thr Met Asp Val Phe Val Lys Glu
3995 4000 4005

Pro Ser Phe Asp Trp Lys Asn Phe Glu Gln Lys Met Leu Lys Lys
4010 4015 4020

Gly Gly Ser Trp Ile Gln Glu Ile Asn Val Ala Glu Lys Asn Trp
4025 4030 4035

Tyr Pro Arg Gln Lys Ile Cys Tyr Ala Lys Arg Lys Leu Ala Gly
4040 4045 4050

Ala Asn Pro Ala Val Ile Thr Cys Asp Glu Leu Leu Leu Gly His
4055 4060 4065

Glu Lys Ala Pro Ala Phe Arg Asp Tyr Val Ala Val Ala Arg Gly
4070 4075 4080

Ser Lys Asp His Asn Ile Arg Ala Gln Glu Pro Glu Ser Gly Leu
4085 4090 4095

Ser Glu Glu Thr Gln Val Lys Cys Leu Met Asp Gln Ala Thr Asp
4100 4105 4110

Pro Asn Ile Leu Gly Arg Thr Trp Glu Gly Trp Glu Pro Trp Met
4115 4120 4125

<210> 4

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)..(21)

<223> HUMAN GENETIC ORIGIN

<220>

<221> MOD_RES

<222> (11)..(11)

<223> PHOSPHORYLATION at T2609

<400> 4

Ser	Thr	Val	Leu	Thr	Pro	Met	Phe	Val	Glu	Thr	Gln	Ala	Ser	Gln	Gly
1				5					10					15	

Thr	Leu	Gln	Thr	Arg
				20

<210> 5

<211> 29

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)..(29)

<223> HUMAN GENETIC ORIGIN

<220>

<221> MOD_RES

<222> (13)..(13)

<223> PHOSPHORYLATION at S2056

<400> 5

Asp	Phe	Ser	Thr	Gly	Val	Gln	Ser	Tyr	Ser	Tyr	Ser	Ser	Gln	Asp	Pro
1				5				10					15		

Arg	Pro	Ala	Thr	Gly	Arg	Phe	Arg	Arg	Arg	Glu	Gln	Arg
				20				25				

<210> 6

<211> 303

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)..(303)
<223> HUMAN GENETIC ORIGIN

<220>
<221> MOD_RES
<222> (177)..(177)
<223> PHOSPHORYLATION at S2056

<400> 6

Met Tyr Ser Arg Leu Pro Lys Asp Asp Val His Ala Lys Glu Ser Lys
1 5 10 15

Ile Asn Gln Val Phe His Gly Ser Cys Ile Thr Glu Gly Asn Glu Leu
20 25 30

Thr Lys Thr Leu Ile Lys Leu Cys Tyr Asp Ala Phe Thr Glu Asn Met
35 40 45

Ala Gly Glu Asn Gln Leu Leu Glu Arg Arg Arg Leu Tyr His Cys Ala
50 55 60

Ala Tyr Asn Cys Ala Ile Ser Val Ile Cys Cys Val Phe Asn Glu Leu
65 70 75 80

Lys Phe Tyr Gln Gly Phe Leu Phe Ser Glu Lys Pro Glu Lys Asn Leu
85 90 95

Leu Ile Phe Glu Asn Leu Ile Asp Leu Lys Arg Arg Tyr Asn Phe Pro
100 105 110

Val Glu Val Glu Val Pro Met Glu Arg Lys Lys Lys Tyr Ile Glu Ile
115 120 125

Arg Lys Glu Ala Arg Glu Ala Ala Asn Gly Asp Ser Asp Gly Pro Ser
130 135 140

Tyr Met Ser Ser Leu Ser Tyr Leu Ala Asp Ser Thr Leu Ser Glu Glu
145 150 155 160

Met Ser Gln Phe Asp Phe Ser Thr Gly Val Gln Ser Tyr Ser Tyr Ser
165 170 175

Ser Gln Asp Pro Arg Pro Ala Thr Gly Arg Phe Arg Arg Arg Glu Gln
180 185 190

Arg Asp Pro Thr Val His Asp Asp Val Leu Glu Leu Glu Met Asp Glu
195 200 205

Leu Asn Arg His Glu Cys Met Ala Pro Leu Thr Ala Leu Val Lys His
210 215 220

Met His Arg Ser Leu Gly Pro Pro Gln Gly Glu Glu Asp Ser Val Pro
225 230 235 240

Arg Asp Leu Pro Ser Trp Met Lys Phe Leu His Gly Lys Leu Gly Asn
245 250 255

Pro Ile Val Pro Leu Asn Ile Arg Leu Phe Leu Ala Lys Leu Val Ile
260 265 270

Asn Thr Glu Glu Val Phe Arg Pro Tyr Ala Lys His Trp Leu Ser Pro
275 280 285

Leu Leu Gln Leu Ala Ala Ser Glu Asn Asn Gly Gly Glu Gly Ile
290 295 300

<210> 7

<211> 388

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)..(388)

<223> HUMAN GENETIC ORIGIN

<220>

<221> MOD_RES

<222> (177)..(177)

<223> PHOSPHORYLATION at S2056

<400> 7

Met Tyr Ser Arg Leu Pro Lys Asp Asp Val His Ala Lys Glu Ser Lys
1 5 10 15

Ile Asn Gln Val Phe His Gly Ser Cys Ile Thr Glu Gly Asn Glu Leu
20 25 30

Thr Lys Thr Leu Ile Lys Leu Cys Tyr Asp Ala Phe Thr Glu Asn Met
35 40 45

Ala Gly Glu Asn Gln Leu Leu Glu Arg Arg Arg Leu Tyr His Cys Ala
50 55 60

Ala Tyr Asn Cys Ala Ile Ser Val Ile Cys Cys Val Phe Asn Glu Leu
65 70 75 80

Lys	Phe	Tyr	Gln	Gly	Phe	Leu	Phe	Ser	Glu	Lys	Pro	Glu	Lys	Asn	Leu	
				85					90					95		
Leu	Ile	Phe	Glu	Asn	Leu	Ile	Asp	Leu	Lys	Arg	Arg	Tyr	Asn	Phe	Pro	
			100					105					110			
Val	Glu	Val	Glu	Val	Pro	Met	Glu	Arg	Lys	Lys	Lys	Tyr	Ile	Glu	Ile	
		115					120					125				
Arg	Lys	Glu	Ala	Arg	Glu	Ala	Ala	Asn	Gly	Asp	Ser	Asp	Gly	Pro	Ser	
	130					135					140					
Tyr	Met	Ser	Ser	Leu	Ser	Tyr	Leu	Ala	Asp	Ser	Thr	Leu	Ser	Glu	Glu	
145					150					155					160	
Met	Ser	Gln	Phe	Asp	Phe	Ser	Thr	Gly	Val	Gln	Ser	Tyr	Ser	Tyr	Ser	
				165					170					175		
Ser	Gln	Asp	Pro	Arg	Pro	Ala	Thr	Gly	Arg	Phe	Arg	Arg	Arg	Glu	Gln	
			180					185						190		
Arg	Asp	Pro	Thr	Val	His	Asp	Asp	Val	Leu	Glu	Leu	Glu	Met	Asp	Glu	
	195						200					205				
Leu	Asn	Arg	His	Glu	Cys	Met	Ala	Pro	Leu	Thr	Ala	Leu	Val	Lys	His	
	210					215					220					
Met	His	Arg	Ser	Leu	Gly	Pro	Pro	Gln	Gly	Glu	Glu	Asp	Ser	Val	Pro	
225					230					235					240	
Arg	Asp	Leu	Pro	Ser	Trp	Met	Lys	Phe	Leu	His	Gly	Lys	Leu	Gly	Asn	
				245					250					255		
Pro	Ile	Val	Pro	Leu	Asn	Ile	Arg	Leu	Phe	Leu	Ala	Lys	Leu	Val	Ile	
		260						265					270			
Asn	Thr	Glu	Glu	Val	Phe	Arg	Pro	Tyr	Ala	Lys	His	Trp	Leu	Ser	Pro	
		275					280					285				
Leu	Leu	Gln	Leu	Ala	Ala	Ser	Glu	Asn	Asn	Gly	Gly	Glu	Gly	Ile	His	
	290					295					300					
Tyr	Met	Val	Val	Glu	Ile	Val	Ala	Thr	Ile	Leu	Ser	Trp	Thr	Gly	Leu	
305					310					315					320	

Ala Thr Pro Thr Gly Val Pro Lys Asp Glu Val Leu Ala Asn Arg Leu
325 330 335

Leu Asn Phe Leu Met Lys His Val Phe His Pro Lys Arg Ala Val Phe
340 345 350

Arg His Asn Leu Glu Ile Ile Lys Thr Leu Val Glu Cys Trp Lys Asp
355 360 365

Cys Leu Ser Ile Pro Tyr Arg Leu Ile Phe Glu Lys Phe Ser Gly Lys
370 375 380

Asp Pro Asn Ser
385

<210> 8

<211> 821

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)..(821)

<223> HUMAN GENETIC ORIGIN

<220>

<221> MOD_RES

<222> (177)..(177)

<223> PHOSPHORYLATION at S2056

<220>

<221> MOD_RES

<222> (730)..(730)

<223> PHOSPHORYLATION at T2609

<400> 8

Met Tyr Ser Arg Leu Pro Lys Asp Asp Val His Ala Lys Glu Ser Lys
1 5 10 15

Ile Asn Gln Val Phe His Gly Ser Cys Ile Thr Glu Gly Asn Glu Leu
20 25 30

Thr Lys Thr Leu Ile Lys Leu Cys Tyr Asp Ala Phe Thr Glu Asn Met
35 40 45

Ala Gly Glu Asn Gln Leu Leu Glu Arg Arg Arg Leu Tyr His Cys Ala
50 55 60

Ala Tyr Asn Cys Ala Ile Ser Val Ile Cys Cys Val Phe Asn Glu Leu

65	70					75					80				
Lys	Phe	Tyr	Gln	Gly	Phe	Leu	Phe	Ser	Glu	Lys	Pro	Glu	Lys	Asn	Leu
			85						90					95	
Leu	Ile	Phe	Glu	Asn	Leu	Ile	Asp	Leu	Lys	Arg	Arg	Tyr	Asn	Phe	Pro
			100					105					110		
Val	Glu	Val	Glu	Val	Pro	Met	Glu	Arg	Lys	Lys	Lys	Tyr	Ile	Glu	Ile
		115					120					125			
Arg	Lys	Glu	Ala	Arg	Glu	Ala	Ala	Asn	Gly	Asp	Ser	Asp	Gly	Pro	Ser
	130					135					140				
Tyr	Met	Ser	Ser	Leu	Ser	Tyr	Leu	Ala	Asp	Ser	Thr	Leu	Ser	Glu	Glu
145					150					155					160
Met	Ser	Gln	Phe	Asp	Phe	Ser	Thr	Gly	Val	Gln	Ser	Tyr	Ser	Tyr	Ser
				165					170					175	
Ser	Gln	Asp	Pro	Arg	Pro	Ala	Thr	Gly	Arg	Phe	Arg	Arg	Arg	Glu	Gln
			180					185						190	
Arg	Asp	Pro	Thr	Val	His	Asp	Asp	Val	Leu	Glu	Leu	Glu	Met	Asp	Glu
	195						200					205			
Leu	Asn	Arg	His	Glu	Cys	Met	Ala	Pro	Leu	Thr	Ala	Leu	Val	Lys	His
	210					215					220				
Met	His	Arg	Ser	Leu	Gly	Pro	Pro	Gln	Gly	Glu	Glu	Asp	Ser	Val	Pro
225					230					235					240
Arg	Asp	Leu	Pro	Ser	Trp	Met	Lys	Phe	Leu	His	Gly	Lys	Leu	Gly	Asn
				245					250					255	
Pro	Ile	Val	Pro	Leu	Asn	Ile	Arg	Leu	Phe	Leu	Ala	Lys	Leu	Val	Ile
			260					265					270		
Asn	Thr	Glu	Glu	Val	Phe	Arg	Pro	Tyr	Ala	Lys	His	Trp	Leu	Ser	Pro
		275					280					285			
Leu	Leu	Gln	Leu	Ala	Ala	Ser	Glu	Asn	Asn	Gly	Gly	Glu	Gly	Ile	His
	290					295					300				
Tyr	Met	Val	Val	Glu	Ile	Val	Ala	Thr	Ile	Leu	Ser	Trp	Thr	Gly	Leu
305					310					315					320

Ala	Thr	Pro	Thr	Gly	Val	Pro	Lys	Asp	Glu	Val	Leu	Ala	Asn	Arg	Leu	
				325					330					335		
Leu	Asn	Phe	Leu	Met	Lys	His	Val	Phe	His	Pro	Lys	Arg	Ala	Val	Phe	
			340					345					350			
Arg	His	Asn	Leu	Glu	Ile	Ile	Lys	Thr	Leu	Val	Glu	Cys	Trp	Lys	Asp	
		355					360					365				
Cys	Leu	Ser	Ile	Pro	Tyr	Arg	Leu	Ile	Phe	Glu	Lys	Phe	Ser	Gly	Lys	
	370					375					380					
Asp	Pro	Asn	Ser	Lys	Asp	Asn	Ser	Val	Gly	Ile	Gln	Leu	Leu	Gly	Ile	
385					390					395					400	
Val	Met	Ala	Asn	Asp	Leu	Pro	Pro	Tyr	Asp	Pro	Gln	Cys	Gly	Ile	Gln	
				405					410					415		
Ser	Ser	Glu	Tyr	Phe	Gln	Ala	Leu	Val	Asn	Asn	Met	Ser	Phe	Val	Arg	
			420					425					430			
Tyr	Lys	Glu	Val	Tyr	Ala	Ala	Ala	Ala	Glu	Val	Leu	Gly	Leu	Ile	Leu	
		435					440					445				
Arg	Tyr	Val	Met	Glu	Arg	Lys	Asn	Ile	Leu	Glu	Glu	Ser	Leu	Cys	Glu	
	450					455					460					
Leu	Val	Ala	Lys	Gln	Leu	Lys	Gln	His	Gln	Asn	Thr	Met	Glu	Asp	Lys	
465					470					475					480	
Phe	Ile	Val	Cys	Leu	Asn	Lys	Val	Thr	Lys	Ser	Phe	Pro	Pro	Leu	Ala	
				485					490					495		
Asp	Arg	Phe	Met	Asn	Ala	Val	Phe	Phe	Leu	Leu	Pro	Lys	Phe	His	Gly	
			500					505					510			
Val	Leu	Lys	Thr	Leu	Cys	Leu	Glu	Val	Val	Leu	Cys	Arg	Val	Glu	Gly	
		515					520					525				
Met	Thr	Glu	Leu	Tyr	Phe	Gln	Leu	Lys	Ser	Lys	Asp	Phe	Val	Gln	Val	
	530					535					540					
Met	Arg	His	Arg	Asp	Asp	Glu	Arg	Gln	Lys	Val	Cys	Leu	Asp	Ile	Ile	
545					550					555					560	

Tyr Lys Met Met Pro Lys Leu Lys Pro Val Glu Leu Arg Glu Leu Leu
565 570 575

Asn Pro Val Val Glu Phe Val Ser His Pro Ser Thr Thr Cys Arg Glu
580 585 590

Gln Met Tyr Asn Ile Leu Met Trp Ile His Asp Asn Tyr Arg Asp Pro
595 600 605

Glu Ser Glu Thr Asp Asn Asp Ser Gln Glu Ile Phe Lys Leu Ala Lys
610 615 620

Asp Val Leu Ile Gln Gly Leu Ile Asp Glu Asn Pro Gly Leu Gln Leu
625 630 635 640

Ile Ile Arg Asn Phe Trp Ser His Glu Thr Arg Leu Pro Ser Asn Thr
645 650 655

Leu Asp Arg Leu Leu Ala Leu Asn Ser Leu Tyr Ser Pro Lys Ile Glu
660 665 670

Val His Phe Leu Ser Leu Ala Thr Asn Phe Leu Leu Glu Met Thr Ser
675 680 685

Met Ser Pro Asp Tyr Pro Asn Pro Met Phe Glu His Pro Leu Ser Glu
690 695 700

Cys Glu Phe Gln Glu Tyr Thr Ile Asp Ser Asp Trp Arg Phe Arg Ser
705 710 715 720

Thr Val Leu Thr Pro Met Phe Val Glu Thr Gln Ala Ser Gln Gly Thr
725 730 735

Leu Gln Thr Arg Thr Gln Glu Gly Ser Leu Ser Ala Arg Trp Pro Val
740 745 750

Ala Gly Gln Ile Arg Ala Thr Gln Gln Gln His Asp Phe Thr Leu Thr
755 760 765

Gln Thr Ala Asp Gly Arg Ser Ser Phe Asp Trp Leu Thr Gly Ser Ser
770 775 780

Thr Asp Pro Leu Val Asp His Thr Ser Pro Ser Ser Asp Ser Leu Leu
785 790 795 800

Phe Ala His Lys Arg Ser Glu Arg Leu Gln Arg Ala Pro Leu Lys Ser
805 810 815

Val Gly Pro Asp Phe
820

<210> 9

<211> 440

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)..(440)

<223> HUMAN GENETIC ORIGIN

<220>

<221> MOD_RES

<222> (349)..(349)

<223> PHOSPHORYLATION at T2609

<400> 9

Ser Gly Lys Asp Pro Asn Ser Lys Asp Asn Ser Val Gly Ile Gln Leu
1 5 10 15

Leu Gly Ile Val Met Ala Asn Asp Leu Pro Pro Tyr Asp Pro Gln Cys
20 25 30

Gly Ile Gln Ser Ser Glu Tyr Phe Gln Ala Leu Val Asn Asn Met Ser
35 40 45

Phe Val Arg Tyr Lys Glu Val Tyr Ala Ala Ala Glu Val Leu Gly
50 55 60

Leu Ile Leu Arg Tyr Val Met Glu Arg Lys Asn Ile Leu Glu Glu Ser
65 70 75 80

Leu Cys Glu Leu Val Ala Lys Gln Leu Lys Gln His Gln Asn Thr Met
85 90 95

Glu Asp Lys Phe Ile Val Cys Leu Asn Lys Val Thr Lys Ser Phe Pro
100 105 110

Pro Leu Ala Asp Arg Phe Met Asn Ala Val Phe Phe Leu Leu Pro Lys
115 120 125

Phe His Gly Val Leu Lys Thr Leu Cys Leu Glu Val Val Leu Cys Arg
130 135 140

Val Glu Gly Met Thr Glu Leu Tyr Phe Gln Leu Lys Ser Lys Asp Phe
145 150 155 160

Val Gln Val Met Arg His Arg Asp Asp Glu Arg Gln Lys Val Cys Leu
165 170 175

Asp Ile Ile Tyr Lys Met Met Pro Lys Leu Lys Pro Val Glu Leu Arg
180 185 190

Glu Leu Leu Asn Pro Val Val Glu Phe Val Ser His Pro Ser Thr Thr
195 200 205

Cys Arg Glu Gln Met Tyr Asn Ile Leu Met Trp Ile His Asp Asn Tyr
210 215 220

Arg Asp Pro Glu Ser Glu Thr Asp Asn Asp Ser Gln Glu Ile Phe Lys
225 230 235 240

Leu Ala Lys Asp Val Leu Ile Gln Gly Leu Ile Asp Glu Asn Pro Gly
245 250 255

Leu Gln Leu Ile Ile Arg Asn Phe Trp Ser His Glu Thr Arg Leu Pro
260 265 270

Ser Asn Thr Leu Asp Arg Leu Leu Ala Leu Asn Ser Leu Tyr Ser Pro
275 280 285

Lys Ile Glu Val His Phe Leu Ser Leu Ala Thr Asn Phe Leu Leu Glu
290 295 300

Met Thr Ser Met Ser Pro Asp Tyr Pro Asn Pro Met Phe Glu His Pro
305 310 315 320

Leu Ser Glu Cys Glu Phe Gln Glu Tyr Thr Ile Asp Ser Asp Trp Arg
325 330 335

Phe Arg Ser Thr Val Leu Thr Pro Met Phe Val Glu Thr Gln Ala Ser
340 345 350

Gln Gly Thr Leu Gln Thr Arg Thr Gln Glu Gly Ser Leu Ser Ala Arg
355 360 365

Trp Pro Val Ala Gly Gln Ile Arg Ala Thr Gln Gln Gln His Asp Phe
370 375 380

Thr Leu Thr Gln Thr Ala Asp Gly Arg Ser Ser Phe Asp Trp Leu Thr
385 390 395 400

Gly Ser Ser Thr Asp Pro Leu Val Asp His Thr Ser Pro Ser Ser Asp
405 410 415

Ser Leu Leu Phe Ala His Lys Arg Ser Glu Arg Leu Gln Arg Ala Pro
420 425 430

Leu Lys Ser Val Gly Pro Asp Phe
435 440

<210> 10
<211> 200
<212> PRT
<213> Artificial Sequence

<220>
<221> PEPTIDE
<222> (1)..(200)
<223> HUMAN GENETIC ORIGIN

<220>
<221> MOD_RES
<222> (109)..(109)
<223> PHOSPHORYLATION at T2609

<400> 10

Leu Ala Lys Asp Val Leu Ile Gln Gly Leu Ile Asp Glu Asn Pro Gly
1 5 10 15

Leu Gln Leu Ile Ile Arg Asn Phe Trp Ser His Glu Thr Arg Leu Pro
20 25 30

Ser Asn Thr Leu Asp Arg Leu Leu Ala Leu Asn Ser Leu Tyr Ser Pro
35 40 45

Lys Ile Glu Val His Phe Leu Ser Leu Ala Thr Asn Phe Leu Leu Glu
50 55 60

Met Thr Ser Met Ser Pro Asp Tyr Pro Asn Pro Met Phe Glu His Pro
65 70 75 80

Leu Ser Glu Cys Glu Phe Gln Glu Tyr Thr Ile Asp Ser Asp Trp Arg
85 90 95

Phe Arg Ser Thr Val Leu Thr Pro Met Phe Val Glu Thr Gln Ala Ser
100 105 110

Gln Gly Thr Leu Gln Thr Arg Thr Gln Glu Gly Ser Leu Ser Ala Arg
115 120 125

Trp Pro Val Ala Gly Gln Ile Arg Ala Thr Gln Gln Gln His Asp Phe
130 135 140

Thr Leu Thr Gln Thr Ala Asp Gly Arg Ser Ser Phe Asp Trp Leu Thr
145 150 155 160

Gly Ser Ser Thr Asp Pro Leu Val Asp His Thr Ser Pro Ser Ser Asp
165 170 175

Ser Leu Leu Phe Ala His Lys Arg Ser Glu Arg Leu Gln Arg Ala Pro
180 185 190

Leu Lys Ser Val Gly Pro Asp Phe
195 200

<210> 11

<211> 428

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)..(428)

<223> HUMAN GENETIC ORIGIN

<220>

<221> MOD_RES

<222> (335)..(335)

<223> PHOSPHORYLATION at T2609

<400> 11

Gln Leu Leu Gly Ile Val Met Ala Asn Asp Leu Pro Pro Tyr Asp Pro
1 5 10 15

Gln Cys Gly Ile Gln Ser Ser Glu Tyr Phe Gln Ala Leu Val Asn Asn
20 25 30

Met Ser Phe Val Arg Tyr Lys Glu Val Tyr Ala Ala Ala Ala Glu Val
35 40 45

Leu Gly Leu Ile Leu Arg Tyr Val Met Glu Arg Lys Asn Ile Leu Glu
50 55 60

Glu Ser Leu Cys Glu Leu Val Ala Lys Gln Leu Lys Gln His Gln Asn
65 70 75 80

Thr Met Glu Asp Lys Phe Ile Val Cys Leu Asn Lys Val Thr Lys Ser
85 90 95

Phe Pro Pro Leu Ala Asp Arg Phe Met Asn Ala Val Phe Phe Leu Leu
100 105 110

Pro Lys Phe His Gly Val Leu Lys Thr Leu Cys Leu Glu Val Val Leu
115 120 125

Cys Arg Val Glu Gly Met Thr Glu Leu Tyr Phe Gln Leu Lys Ser Lys
130 135 140

Asp Phe Val Gln Val Met Arg His Arg Asp Asp Glu Arg Gln Lys Val
145 150 155 160

Cys Leu Asp Ile Ile Tyr Lys Met Met Pro Lys Leu Lys Pro Val Glu
165 170 175

Leu Arg Glu Leu Leu Asn Pro Val Val Glu Phe Val Ser His Pro Ser
180 185 190

Thr Thr Cys Arg Glu Gln Met Tyr Asn Ile Leu Met Trp Ile His Asp
195 200 205

Asn Tyr Arg Asp Pro Glu Ser Glu Thr Asp Asn Asp Ser Gln Glu Ile
210 215 220

Phe Lys Leu Ala Lys Asp Val Leu Ile Gln Gly Leu Ile Asp Glu Asn
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Pro Gly Leu Gln Leu Ile Ile Arg Asn Phe Trp Ser His Glu Thr Arg
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Leu Pro Ser Asn Thr Leu Asp Arg Leu Leu Ala Leu Asn Ser Leu Tyr
260 265 270

Ser Pro Lys Ile Glu Val His Phe Leu Ser Leu Ala Thr Asn Phe Leu
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Leu Glu Met Thr Ser Met Ser Pro Asp Tyr Pro Asn Pro Met Phe Glu
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His Pro Leu Ser Glu Cys Glu Phe Gln Glu Tyr Thr Ile Asp Ser Asp
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Trp Arg Phe Arg Ser Thr Val Leu Thr Pro Met Phe Val Glu Thr Gln
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Ala Ser Gln Gly Thr Leu Gln Thr Arg Thr Gln Glu Gly Ser Leu Ser
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Ala Arg Trp Pro Val Ala Gly Gln Ile Arg Ala Thr Gln Gln Gln His
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Asp Phe Thr Leu Thr Gln Thr Ala Asp Gly Arg Ser Ser Phe Asp Trp
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Met Trp Ile His Asp Asn Tyr Arg Asp Pro Glu Ser Glu Thr Asp Asn
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Asp Ser Gln Glu Ile Phe Lys Leu Ala Lys Asp Val Leu Ile Gln Gly
65 70 75 80

Leu Ile Asp Glu Asn Pro Gly Leu Gln Leu Ile Ile Arg Asn Phe Trp
85 90 95

Ser His Glu Thr Arg Leu Pro Ser Asn Thr Leu Asp Arg Leu Leu Ala
100 105 110

Leu Asn Ser Leu Tyr Ser Pro Lys Ile Glu Val His Phe Leu Ser Leu
115 120 125

Ala Thr Asn Phe Leu Leu Glu Met Thr Ser Met Ser Pro Asp Tyr Pro
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Asn Pro Met Phe Glu His Pro Leu Ser Glu Cys Glu Phe Gln Glu Tyr
145 150 155 160

Thr Ile Asp Ser Asp Trp Arg Phe Arg Ser Thr Val Leu Thr Pro Met
165 170 175

Phe Val Glu Thr Gln Ala Ser Gln Gly Thr Leu Gln Thr Arg Thr Gln
180 185 190

Glu Gly Ser Leu Ser Ala Arg Trp Pro Val Ala Gly Gln Ile Arg Ala
195 200 205

Thr Gln Gln Gln His Asp Phe Thr Leu Thr Gln Thr Ala Asp Gly Arg
210 215 220

Ser Ser Phe Asp Trp Leu Thr Gly Ser Ser Thr Asp Pro Leu Val Asp
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His Thr Ser Pro Ser Ser Asp Ser Leu Leu Phe Ala His Lys Arg Ser
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Glu Arg Leu Gln Arg Ala Pro Leu Lys Ser Val Gly Pro Asp Phe Gly
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Lys

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Thr Gln Ala Ser Gln Gly Thr Leu Gln Thr Arg Thr Gln Glu Gly Ser
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Leu Ser Ala Arg Trp Pro Val Ala Gly Gln Ile Arg Ala Thr Gln Gln
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Gln His Asp Phe Thr Leu Thr Gln Thr Ala Asp Gly Arg Ser Ser Phe
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Asp Trp Leu Thr Gly Ser Ser Thr Asp Pro Leu Val Asp His Thr Ser
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Gly Gln Ile Arg Ala Thr Gln Gln Gln His Asp Phe Thr Leu Thr Gln
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Thr Ala Asp Gly Arg Ser Ser Phe Asp Trp Leu Thr Gly Ser Ser Thr
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Asp Pro Leu Val Asp His Thr Ser Pro Ser Ser Asp Ser Leu Leu Phe
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<210> 16

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> cDNA sequence encoding the 2599-2619 peptide

<220>

<221> CDS

<222> (1)..(63)

<223> HUMAN GENETIC ORIGIN

<220>

<221> misc_feature

<222> (31)..(33)

<223> encodes T2609 residue

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cgt 63

<210> 17

<211> 87

<212> DNA

<213> Artificial sequence

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<223> cDNA sequence encoding the 2044-2072 peptide

<220>

<221> CDS

<222> (1)..(87)

<223> HUMAN GENETIC ORIGIN

<220>

<221> misc_feature

<222> (37)..(37)

<223> encodes S2056 residue

<400> 17

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ggtcgtttttc ggagacggga gcagcgg 87

<210> 18

<211> 909

<212> DNA

<213> Artificial Sequence

<220>

<223> cDNA sequence encoding the 1879-2182 peptide

<220>

<221> CDS

<222> (1)..(909)

<223> HUMAN GENETIC ORIGIN

<220>

<221> misc_feature

<222> (529)..(529)

<223> encodes S2056 residue

<400> 18

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tacgatgcat ttacagagaa catggcagga gagaatcagc tgctggagag gagaagactt 180

taccattgtg cagcatacaa ctgcgccata tctgtcatct gctgtgtctt caatgagtta 240

aaattttacc aaggttttct gtttagtgaa aaaccagaaa agaacttgct tatttttgaa 300

aatctgatcg acctgaagcg ccgctataat ttctctgtag aagttgaggt tcctatggaa 360

agaaagaaaa agtacattga aattaggaaa gaagccagag aagcagcaaa tggggattca 420

gatggtcctt cctatatgtc ttccctgtca tatttggcag acagtaccct gagtgaggaa 480

atgagtcaat ttgatttctc aaccggagtt cagagctatt catacagctc ccaagaccct 540

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gtgctggagc tggagatgga cgagctcaat cggcatgagt gcatggcgcc cctgacggcc 660

ctggtcaagc acatgcacag aagcctgggc ccgcctcaag gagaagagga ttcagtgcc 720

agagatcttc cttcttggtat gaaattcctc catggcaaac tgggaaatcc aatagtacca 780

ttaaataatcc gtctcttctt agccaagctt gttattaata cagaagaggt ctttcgcct 840

tacgcgaagc actggcttag ccccttgctg cagctggctg cttctgaaaa caatggagga 900

gaaggaatt 909

<210> 19

<211> 1164

<212> DNA

<213> Artificial sequence

<220>

<223> Cloned DNA sequence encoding the 1879-2267 peptide

<220>

<221> CDS

<222> (1)..(1164)

<223> HUMAN GENETIC ORIGIN

<220>

<221> misc_feature

<222> (529)..(531)

<223> encodes S2056 residue

<400> 19

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tacgatgcat ttacagagaa catggcagga gagaatcagc tgctggagag gagaagactt      180
taccattgtg cagcatacaa ctgcgccata tctgtcatct gctgtgtctt caatgagtta      240
aaattttacc aaggttttct gtttagtgaa aaaccagaaa agaacttgct tatttttgaa      300
aatctgatcg acctgaagcg ccgctataat tttcctgtag aagttgaggt tcctatggaa      360
agaaagaaaa agtacattga aattaggaaa gaagccagag aagcagcaaa tggggattca      420
gatggtcctt cctatatgtc ttccctgtca tatttggcag acagtaccct gagtgaggaa      480
atgagtcaat ttgatttctc aaccggagtt cagagctatt catacagctc ccaagaccct      540
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atgaaacatg tctttcatcc aaaaagagct gtgttttagac acaaccttga aattataaag     1080
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ttttccggtg aagatcctaa ttct

1164

<210> 20

<211> 2463

<212> DNA

<213> Artificial Sequence

<220>

<223> cDNA sequence encoding the 1879-2700 peptide

<220>

<221> CDS

<222> (1)..(2463)

<223> HUMAN GENETIC ORIGIN

<220>

<221> misc_feature

<222> (529)..(531)

<223> encodes S2056 residue

<220>

<221> misc_feature

<222> (2188)..(2190)

<223> encodes T2609 residue

<400> 20

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tacgatgcat ttacagagaa catggcagga gagaatcagc tgctggagag gagaagactt	180
taccattgtg cagcatacaa ctgcgccata tctgtcatct gctgtgtctt caatgagtta	240
aaattttacc aaggttttct gtttagtgaa aaaccagaaa agaacttgct tatttttgaa	300
aatctgatcg acctgaagcg ccgctataat ttctctgtag aagttgaggt tcctatggaa	360
agaaagaaaa agtacattga aattaggaaa gaagccagag aagcagcaaa tggggattca	420
gatggtcctt cctatatgtc ttccctgtca tttttggcag acagtaacct gagtgaggaa	480
atgagtcaat ttgatttctc aaccggaggt cagagctatt catacagctc ccaagaccct	540
agacctgcca ctggtcgttt tcggagacgg gagcagcggg accccacggt gcatgatgat	600
gtgctggagc tggagatgga cgagctcaat cggcatgagt gcatggcgcc cctgacggcc	660
ctgggtcaagc acatgcacag aagcctgggc ccgcctcaag gagaagagga ttcagtgcc	720
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ttt	2463

<210> 21

<211> 1320

<212> DNA

<213> Artificial sequence

<220>

<223> cDNA sequence encoding the 2261-2700 peptide

<220>

<221> CDS

<222> (1)..(1320)

<223> HUMAN GENETIC ORIGIN

<220>

<221> misc_feature

<222> (1045)..(1047)

<223> encodes T2609 residue

<400> 21

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atggccaatg acctgcctcc ctatgaccca cagtgtggca tccagagtag cgaatacttc      120
caggcttttg tgaataatat gtcctttgta agatataaag aagtgtatgc cgctgcagca      180
gaagttctag gacttatact tcgatatggt atggagagaa aaaacatact ggaggagtct      240
ctgtgtgaac tggttgcgaa acaattgaag caacatcaga atactatgga ggacaagttt      300
attgtgtgct tgaacaaagt gaccaagagc ttccctcctc ttgcagacag gttcatgaat      360
gctgtgttct ttctgctgcc aaaatttcat ggagtgttga aaacactctg tctggagggtg      420
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ctgtcagaat gcgaatttca ggaatatacc attgattctg attggcgttt ccgaagtact     1020
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gggagcagca ctgaccgct ggtcgaccac accagtcctt catctgactc cttgctgttt     1260
gccacaaga ggagtgaag gttacagaga gcacccttga agtcagtggg gcctgatttt     1320
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<210> 22

<211> 600
<212> DNA
<213> Artificial Sequence

<220>

<223> cDNA sequence encoding the 2500-2700 peptide

<220>

<221> CDS

<222> (1)..(600)

<223> HUMAN GENETIC ORIGIN

<220>

<221> misc_feature

<222> (325)..(327)

<223> encodes T2609 residue

<400> 22

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ttggcaaaag atgtgctgat tcaaggattg atcgatgaga accctggact tcaattaatt      60
attcgaaatt tctggagcca tgaaactagg ttaccttcaa ataccttgga ccggttgctg     120
gcactaaatt ccttatattc tcctaagata gaagtgcact ttttaagttt agcaacaaat     180
tttctgctcg aaatgaccag catgagccca gattatccaa accccatggt cgagcatcct     240
ctgtcagaat gcgaatttca ggaatatacc attgattctg attggcgttt ccgaagtact     300
gttctcactc cgatgtttgt ggagaccag gcctcccagg gcactctcca gaccogtacc     360
caggaagggt ccctctcagc tcgctggcca gtggcagggc agataagggc caccagcag      420
cagcatgact tcacactgac acagactgca gatggaagaa gctcatttga ttggctgacc     480
gggagcagca ctgaccogct ggtcgaccac accagtcctt catctgactc cttgctgttt     540
gccacaaga ggagtgaaag gttacagaga gcacccttga agtcagtggg gcctgatttt     600
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<210> 23

<211> 1284

<212> DNA

<213> Artificial sequence

<220>

<223> cDNA sequence encoding 2275-2702 peptide

<220>

<221> CDS

<222> (1)..(1284)

<223> HUMAN GENETIC ORIGIN

<220>

<221> misc_feature

<222> (1003)..(1005)

<223> encodes T2609 residue

<400> 23

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gtgtatgccg ctgcagcaga agttctagga cttatacttc gatatgttat ggagagaaaa	180
aacatactgg aggagtctct gtgtgaactg gttgcgaaac aattgaagca acatcagaat	240
actatggagg acaagtttat tgtgtgcttg aacaaagtga ccaagagctt ccctcctctt	300
gcagacaggt tcatgaatgc tgtgttcttt ctgctgccaa aatttcatgg agtggtgaaa	360
acactctgtc tggaggtggt actttgtcgt gtggagggaa tgacagagct gtacttccag	420
ttaaagagca aggacttcgt tcaagtcatg agacatagag atgatgaaag aaaaaagta	480
tgtttggaca taatttataa gatgatgcca aagttaaaac cagtagaact ccgagaactt	540
ctgaaccccg ttgtggaatt cgtttcccat ccttctacaa catgtaggga acaaatgtat	600
aatattctca tgtggattca tgataattac agagatccag aaagtgagac agataatgac	660
tcccaggaaa tatttaagtt ggcaaaagat gtgctgattc aaggattgat cgatgagaac	720
cctggacttc aattaattat tcgaaatttc tggagccatg aaactagggt accttcaa	780
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ttaagtttag caacaaattt tctgctcgaa atgaccagca tgagcccaga ttatccaaac	900
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ataagggcca cccagcagca gcatgacttc aactgacac agactgcaga tggaagaagc	1140
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tctgactcct tgctgtttgc ccacaagagg agtgaaaggt tacagagagc acccttgaag	1260
tcagtggggc ctgattttgg gaaa	1284

<210> 24

<211> 819

<212> DNA

<213> Artificial Sequence

<220>

<223> cDNA sequence encoding 2429-2072 peptide

<220>

<221> CDS

<222> (1)..(819)

<223> HUMAN GENETIC ORIGIN

<220>

<221> misc_feature

<222> (538)..(540)
<223> encodes T2609 residue

<400> 24

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gaaagacaaa aagtatgttt ggacataatt tataagatga tgccaaagtt aaaaccagta      60
gaactccgag aacttctgaa ccccgttgtg gaattcgttt cccatccttc tacaacatgt      120
agggaacaaa tgtataatat tctcatgtgg attcatgata attacagaga tccagaaagt      180
gagacagata atgactccca ggaaatatat aagttggcaa aagatgtgct gattcaagga      240
ttgatcgatg agaaccctgg acttcaatta attattcgaa atttctggag ccatgaaact      300
aggttacctt caaatacctt ggaccggttg ctggcactaa attccttata ttctcctaag      360
atagaagtgc actttttaag tttagcaaca aattttctgc tcgaaatgac cagcatgagc      420
ccagattatc caaaccccat gttcgagcat cctctgtcag aatgcgaatt tcaggaatat      480
accattgatt ctgattggcg tttccgaagt actgttctca ctccgatgtt tgtggagacc      540
caggcctccc agggcactct ccagaccctg acccaggaag ggtccctctc agctcgctgg      600
ccagtggcag ggcagataag ggccaccag cagcagcatg acttcacact gacacagact      660
gcagatggaa gaagctcatt tgattggctg accgggagca gcaactgacc gctggctgac      720
cacaccagtc cctcatctga ctcttgctg tttgccaca agaggagtga aaggttacag      780
agagcacctt tgaagtcagt ggggcctgat tttgggaaa      819
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<210> 25

<211> 420
<212> DNA
<213> Artificial Sequence

<220>
<223> cDNA Sequence encoding 2561-2700 peptide

<220>
<221> CDS
<222> (1)..(420)
<223> HUMAN GENETIC ORIGIN

<220>
<221> misc_feature
<222> (145)..(147)
<223> Encodes T2609 residue

<400> 25

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tttctgctcg aaatgaccag catgagccca gattatccaa accccatgtt cgagcatcct      60
ctgtcagaat gcgaatttca ggaatatacc attgattctg attggcgttt ccgaagtact      120
gttctcactc cgatgtttgt ggagaccag gcctcccagg gcactctcca gaccgtacc      180
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caggaagggt ccctctcagc tcgctggcca gtggcagggc agataagggc caccagcag	240
cagcatgact tcacactgac acagactgca gatggaagaa gctcatttga ttggctgacc	300
gggagcagca ctgacccgct ggtcgaccac accagtcctt catctgactc cttgctgttt	360
gccacaaga ggagtgaag gttacagaga gcacccttga agtcagtggg gcctgatttt	420

<210> 26

<211> 306

<212> DNA

<213> Artificial Sequence

<220>

<223> cDNA sequence encoding 2600-2702 peptide

<220>

<221> CDS

<222> (1)..(306)

<223> HUMAN GENETIC ORIGIN

<220>

<221> misc_feature

<222> (25)..(27)

<223> Encodes T2609 residue

<400> 26

gttctcactc cgatgtttgt ggagaccag gcctcccagg gcaactctcca gaccggtacc	60
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cagcatgact tcacactgac acagactgca gatggaagaa gctcatttga ttggctgacc	180
gggagcagca ctgacccgct ggtcgaccac accagtcctt catctgactc cttgctgttt	240
gccacaaga ggagtgaag gttacagaga gcacccttga agtcagtggg gcctgatttt	300
gggaaa	306

<210> 27

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Primer to create T2609A mutation

<400> 27

tccgatgttt gtggaggacc aggcctccca gggc	34
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<210> 28

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Reverse primer to create T2609A mutation

<400> 28

gccctgggag gcctggcct ccacaaacat cgga

34